

FIGURE 1

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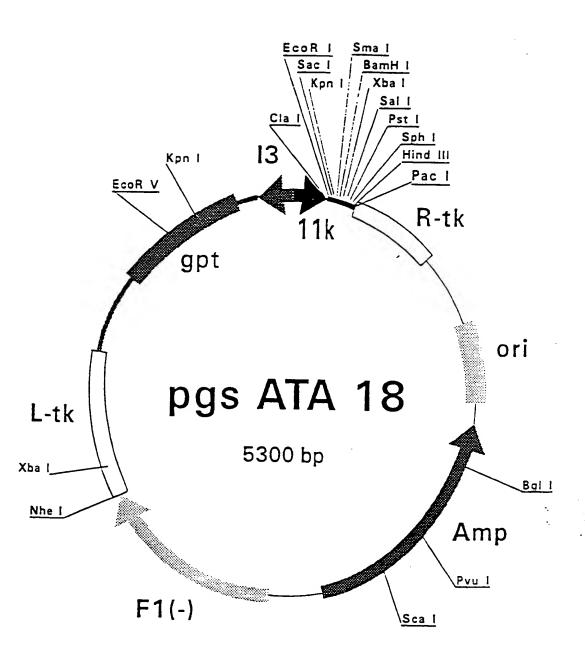


FIGURE 2

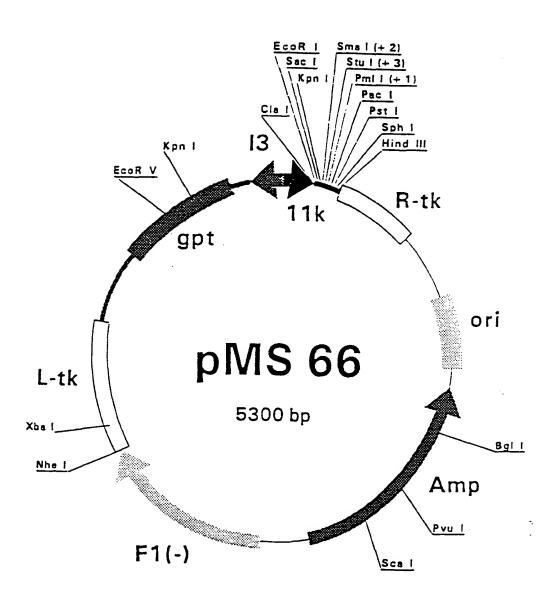


FIGURE 3

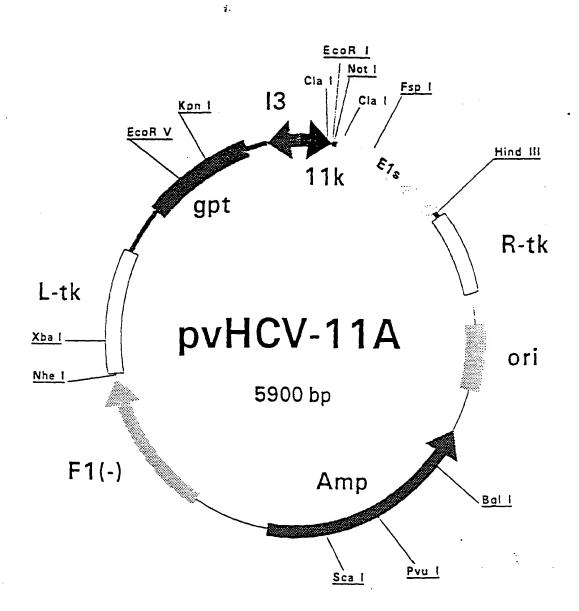
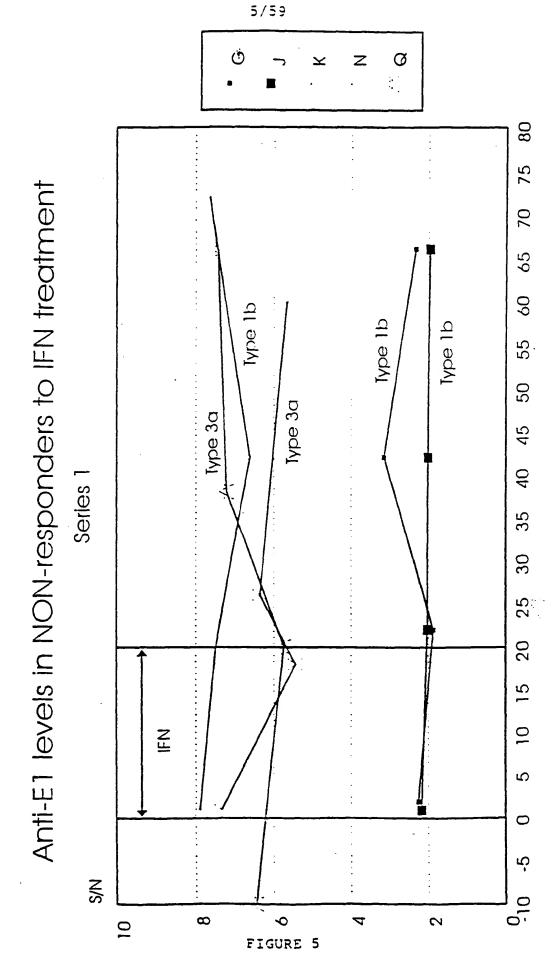


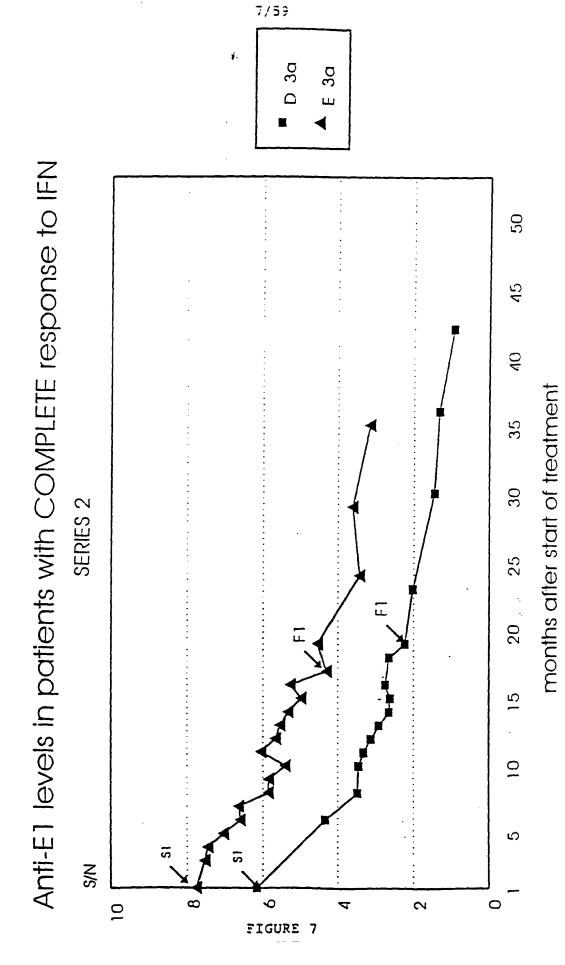
FIGURE 4



weeks after start of treatment

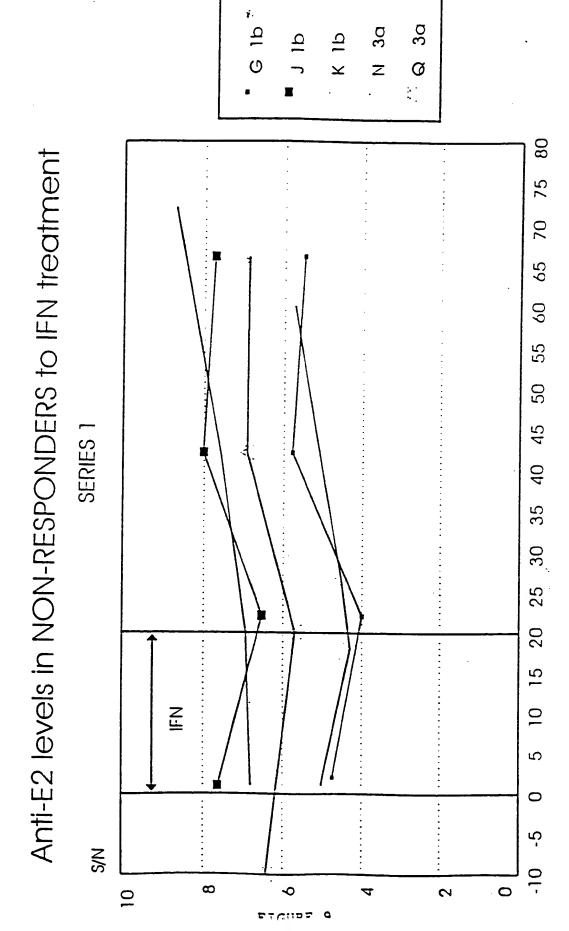
weeks after start of treatment

Σ ے 80 70 Anti-E1 levels in RESPONDERS to IFN treatment 9 50 40 SERIES 1 30 20 10 FN 0 S/N 0 ထ 9 2 10 4 2

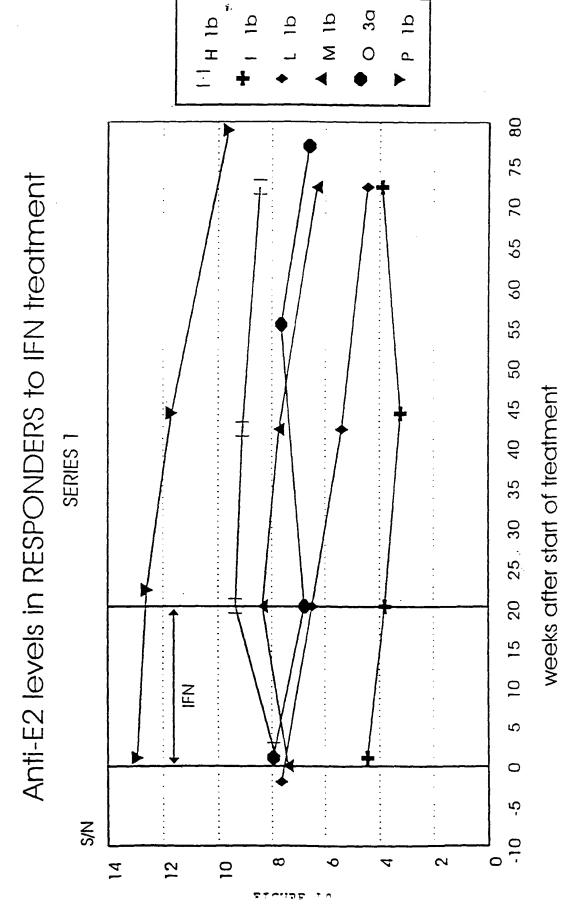


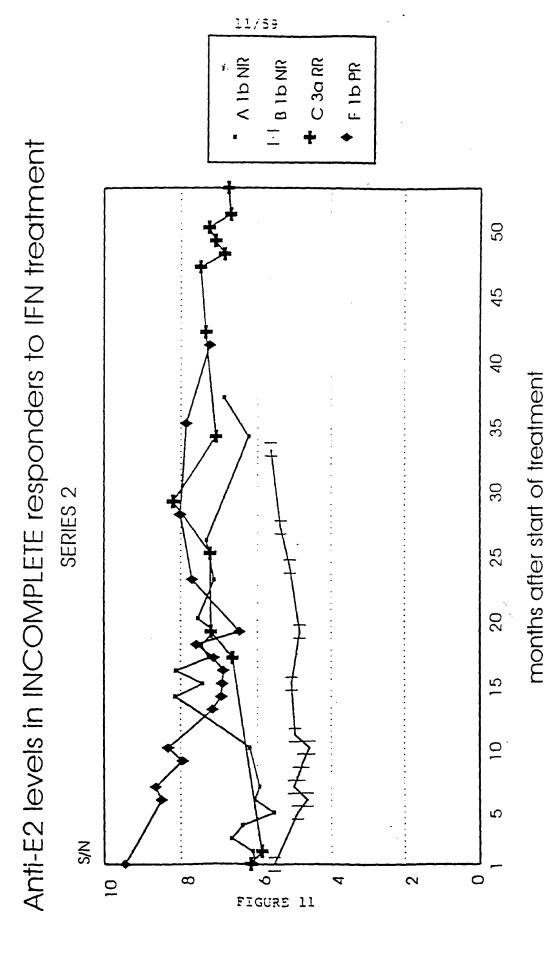
months after start of treatment

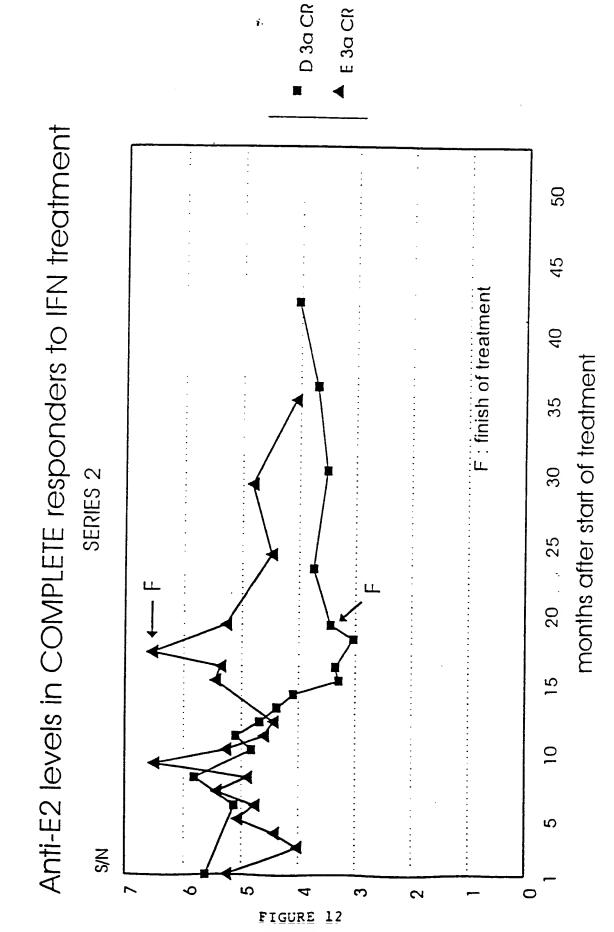
A 15 NR I.I BIDNR 🛨 C 3a RR F 15 PR Anti-E1 levels in INCOMPLETE responders to IFN treatment 50 **S**2 45 F: finish of treatment S: start of treatment 40 35 30 SERIES 2 25 20 15 10 ī S/N 5 2 S C FIGURE 01 α ထ 9 2 0 ∀ 7



weeks after start of treatment



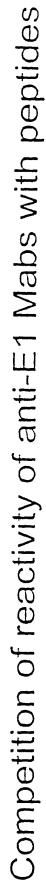


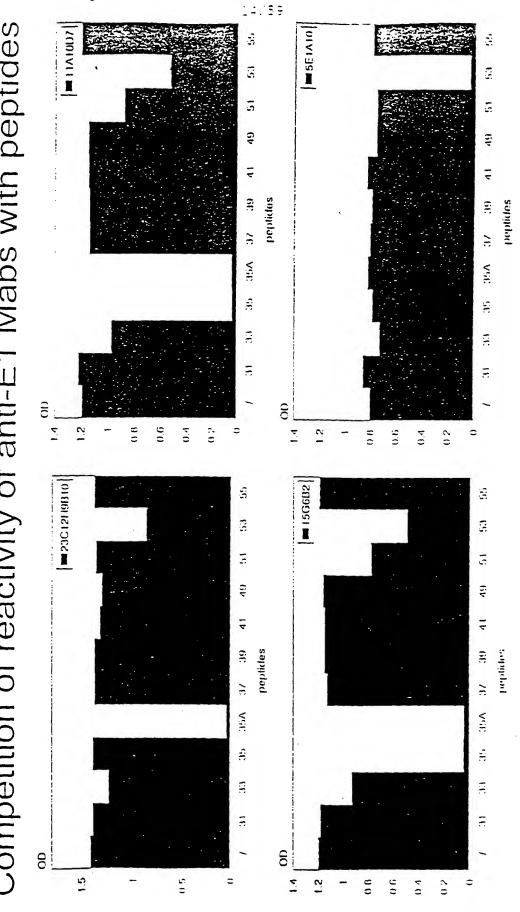


■1G10919 In the peptide mix 1 1 competed with peptide mix 1630240 Human anti-E1 reactivity competed with peptides 55 160332 3 5 IG10919 IG10907 45 human sera 5 peptides 39 0.5250 37 357 1G10925 1G5202 33 8 00 00 8 0.5 C: 0 3 0.0 = 9.0 0.4 0.2 **■** IG8248 **■**1G5250 55 Ş 23 3 5 5 45 peptides poptidos 37 ? 354 35 35 33 Ξ 33 Ξ Ξ 90 = 0.8 2 0.5 0.8

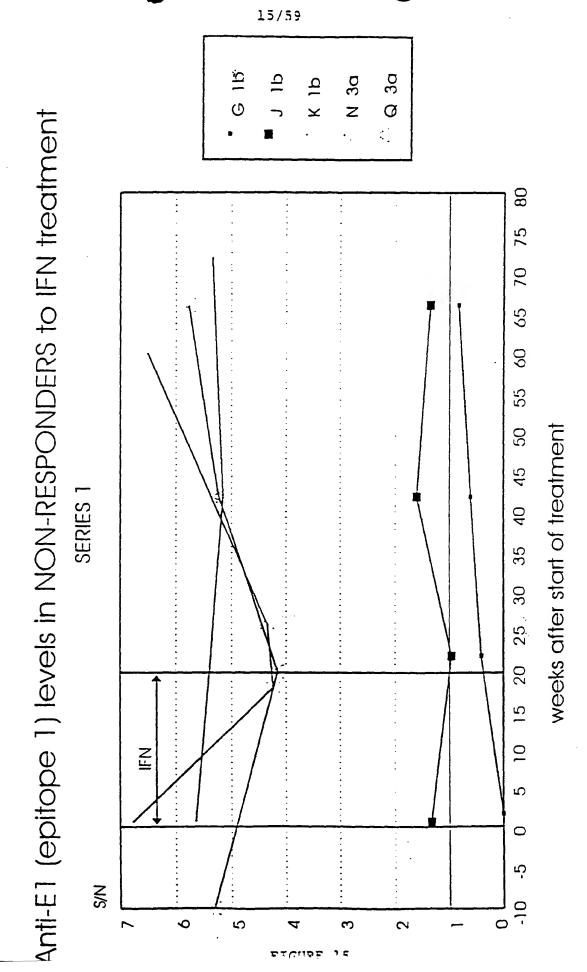
13,59

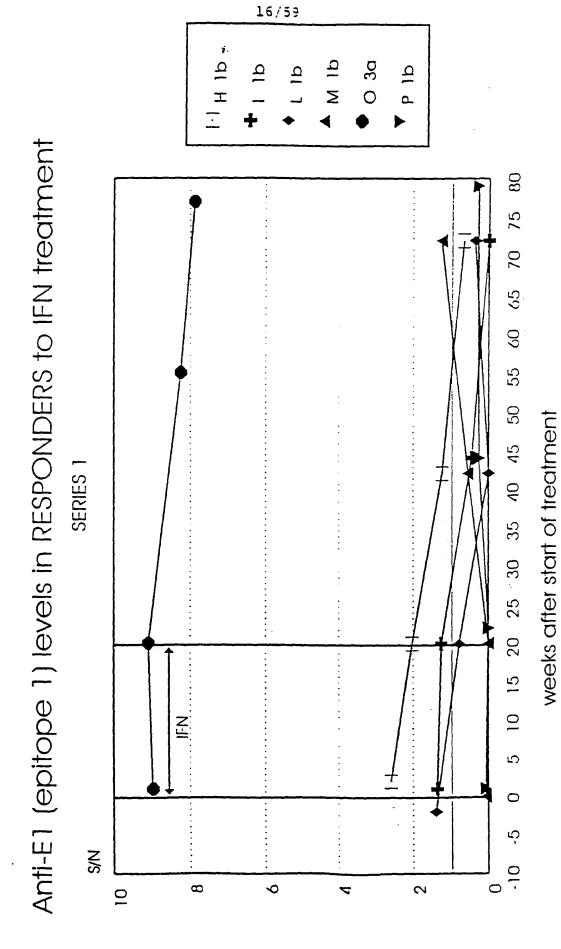
FIGURE 14

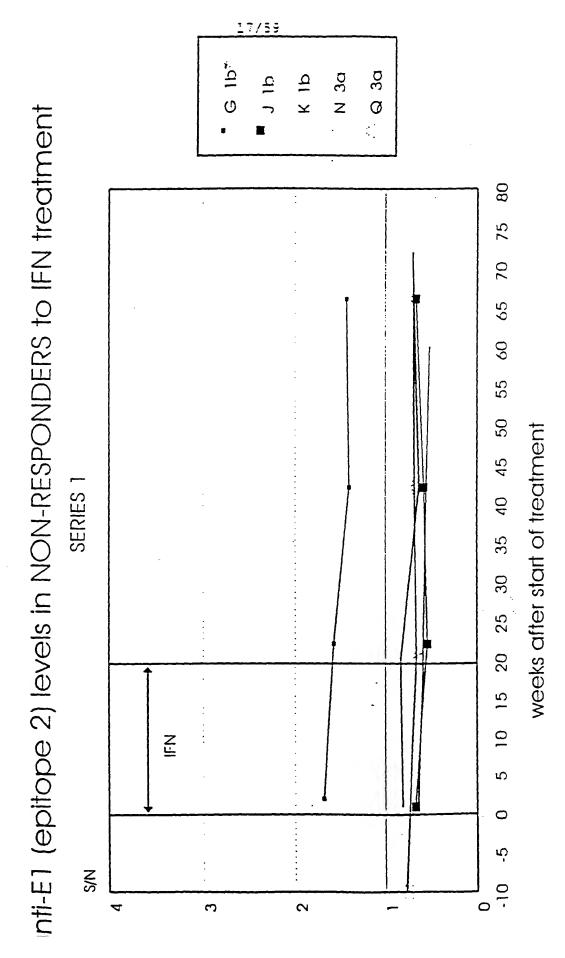


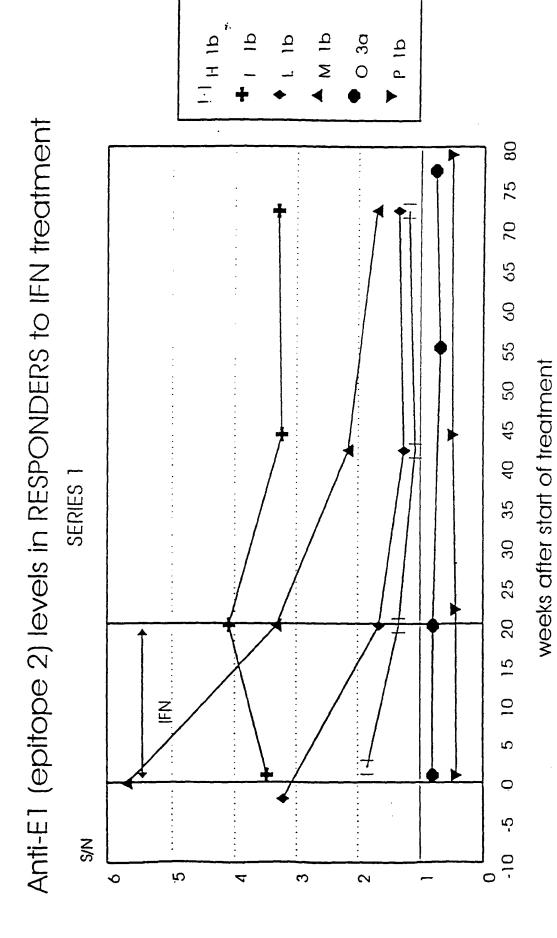












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FIGURE 19 Competition of reactivity of anti-E2 Mabs with peptides 16A6E7 26: 82. 88. 88. 88. populates 3. 3. 33 ≘. 33B 3.3 69 -5 53 5 0.5 - 2F 101110 ÷2 30 30 30 5Z .:Z **5**E Œ -2 36: 944 populatos 39; 38: 3:: 35 34 23 **=**: Ξ: 533 : :: 3 ê 5 .-= 1.5 =

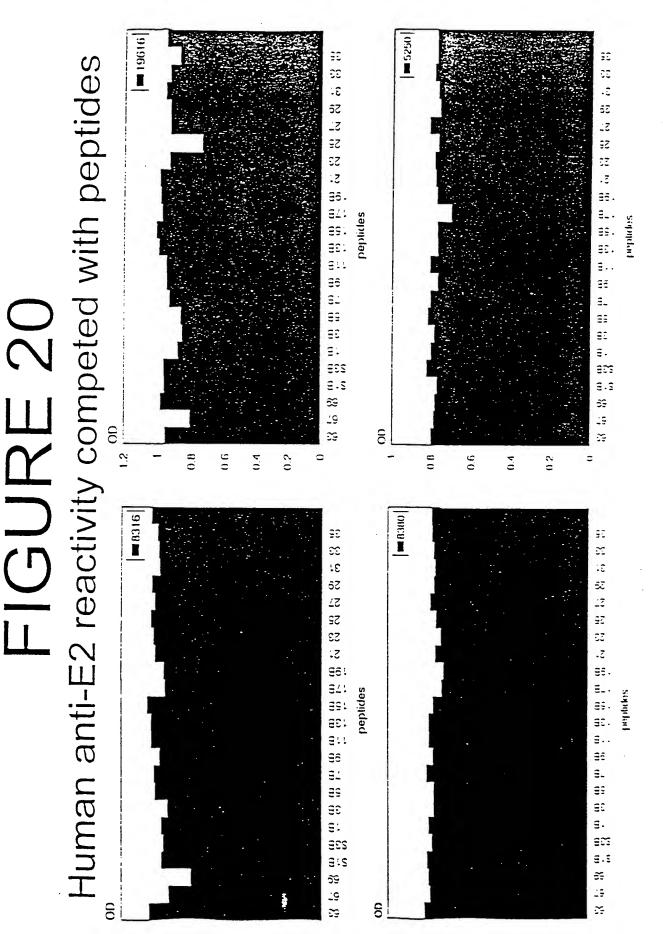


Figure 21

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)
3'ACGTCCGTACGTTCGAATTAATTAATCGA5' (SEQ ID NO 94)

SEQ ID NO 3 (HCCI9A)

SEQ ID NO 5 (HCCI10A)



SEQ ID NO 7 (HCCI11A)

SEQ ID NO 9 (HCCI12A)

SEQ ID NO 11 (HCCI13A)



GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTC
GTTGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCTGTTTT
CCTTGTTTCCCAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

SEQ ID NO 13 (HCCI17A)

SEQ ID NO 15 (HCPr51)

ATGCCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCPr52)

ATGTTGGGTAAGGTCATCGATACCCT

SEQ ID NO 17 (HCPr53)
CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCPr54)
CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPr107)

ATACGACGCCACGTCGATTCCCAGCTGTTCACCATC

SEQ ID NO 20 (HCPr108)
GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCCI37)

SEQ ID NO 23 (HCCI38)

SEQ ID NO 25 (HCC139)

TAG

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTCTCT





CAACGTGTCCGGGATGTACCATGTCACGAACGACTCCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACCCCCGGGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCG
CCGGCATGAGACGGCGAGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGTAT
CGCAGCTGCTCCGGATCCTCAATAG

SEQ ID NO 27 (HCCI40)

SEQ ID NO 29 (HCCI62)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCC CGCTCGTAGGCGGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGT CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT TTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATG

CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCA GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC GGCTCCTCTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG TTATACGTAGGAGACGCGTGTGGGGCCACTATTCTTGGTAGGCCAAATGTTCACCTATA GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT

TACCGGCCACCGGATGGCATGGGATATGATGACTGGTAATAG

TGGGATATGATGATGAACTGGTC

SEQ ID NO 33 (HCPr109)

SEQ ID NO 34 (HCPr72)

CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

TGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCC GGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGG GCCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTC TTTGCCGGCGTCGACGGGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGGCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCACCTCTCACGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCCTTCACCACCCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTGTAGG
GTCGGCGGTTGTCTCCCTTGTCATCAAATGGGAGTATGTCCTGTTGCTCTTCCTT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTCGATAGCTCAAGCTGAG
GCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGC
ACTCTTTCCTTCCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGTCCC
TGGTGCGGCATACGCCTTCTTATGGCGTCTGCCTGCTTCTGCTGCCTTAC
CACCACGAGCTTATGCCTAGTAA

SEC ID NO 37 (HCCI41)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGG CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGATGCTACTCT TTGCCGGCGTCGACGGGCATACCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGTGCGTCCAGTGTATTGCTTCACCCCGAGCC CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGGCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGGGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG TCTACAACAGAGTGGCAGAGTTAATTAATTAG

SEQ ID NO 39 (HCC142)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGGG CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT

AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG

TCTACAACAGGTGATCGAGGGCAGACACCATCACCATCACTAATAG

SEQ ID NO 41 (HCCI43)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC ATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGG CAGAGCTTAATTAATTAG



SEQ ID NO 43 (HCC144)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAACACACAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAGGTTCGCTGAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG ATTCTCAACACACGCGGCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACETTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGTCTACAACAGGTGAT CGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 45 (HCCL64)

TGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGA
GGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATA
CTGCCCTGTTCCTTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCA
GAACATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTC
ATCAAATGGGAGTATGTCCTGTTGCTCTTCCTTCTCCTGGCAGACGCGCGCATCTGCGC
CTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTG
GTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGCCCTTCTTC
CTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGCCATACGCCTTCTAT
GGCGTGTGGCCGCTGCTCCTGCTTCTCTTCCTTAGCCTAGTAA

SEQ ID NO 47 (HCCI65)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT GAGGCAGCGGACATGATCATGCACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATCTATCCCGG CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACG GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG GGGCCCATTGGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGC TAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGTGTCAG GAGGGGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGC TCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACTGCCCT GAACTGCAACGACTCCCCAAACAGGGTTCTTTGCCGCACTATTCTACAAACACAAA TTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCG CTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGGCCCTA CTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT CCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGGACGACCGATCGGTTTGGTGT CCCCACGTATAACTGGGGGGGGAACGACTCGGATGTGCTGATTCTCAACAACACGCGG CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCACCAAGA CGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGACCTGCC

SEQ ID NO 49 (HCC166)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCA CAGGACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGC GCAGGGGCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAAC CTCGTGGGAGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGG CTCAGCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATG GCTCCTGTCACCCGCGGCTCTCGGCCTAGTTGGGGCCCTACAGACCCCCGGCGTAGG TCGCGTAATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGG GGTACATTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG CGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCT TTCTCTATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAA GTGCGCAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTG GAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCC AGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTT TCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTG TTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATC CCGGCCACATAACGGGTCACCGTATGGCTTGGGATATGATGAACTGGTCGCCTAC AACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTG GCGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACT GGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGT GTCAGGAGGGGCAGCCTCCGATACCAGGGCCTTGTGTCCCTCTTTAGCCCCGGG

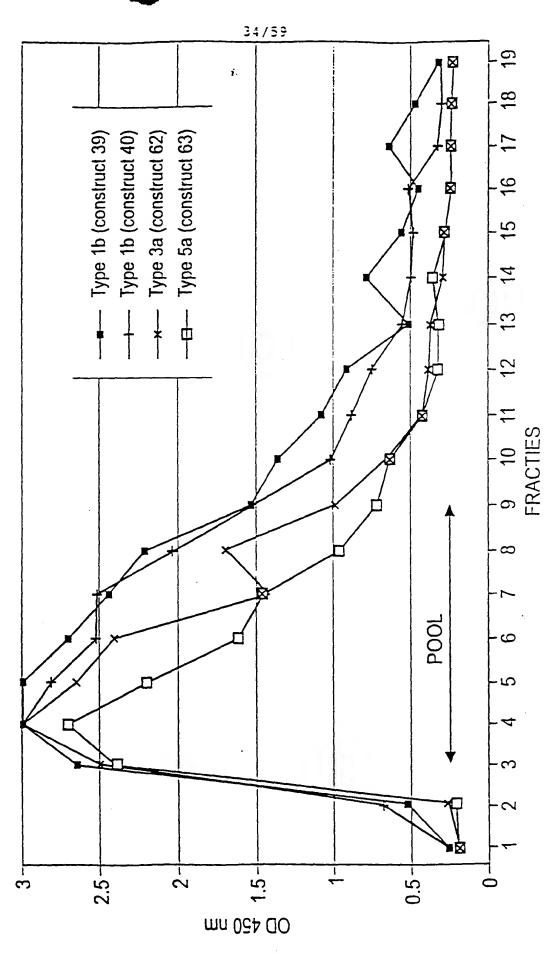
TCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT GCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAAC ACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAA GTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGT GCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTT TGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAAC ACGCGGCCGCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCA CCAAGACGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGA CCTGCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTC TGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTAC ACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACA GGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCC CTGTTCCTTCACCACCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC ATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTCATCA AATGGGAGTATGTCCTGTTGCTCTTCTTCTCCTGGCAGACGCGCGCATCTGCGCCTGC TTATGGATGATGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCC GCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCTTCTATGGCG TGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA

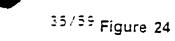


Figure 22

OD measured at 450 nm construct

Fraction	volume dilution	39 Typ e Ib	40 Type Ih	62 Type 3a	63 Type 5a
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	23 ml 1/20 PUGH 23 ml 1/20 0.4 ml 1/200	2.517 0.087 0.102 0.395 2.627 3 3 2.694 2.408 2.176 1.461 1.286 0.981 0.812 0.812 0.373 0.653 0.441 0.321 0.525 0.331	1.954 0.085 0.051 0.550 2.603 2.967 2.810 2.499 2.481 1.970 1.422 0.926 0.781 0.650 0.432 0.371 0.348 0.374 0.186 0.171	1.426 0.176 0.048 0.090 2.481 3 2.640 1.359 0.347 1.624 0.887 0.543 0.294 0.249 0.239 0.145 0.151 0.098 0.099 0.083	1.142 0.120 0.050 0.067 2.372 2.694 2.154 1.561 1.390 0.865 0.604 0.519 0.294 0.199 0.209 0.184 0.151 0.106 0.108 0.090
19		0.192	0.164	0.084	0.087





Fraction	volume	dilution		sured at 450 nstruct 40 Type 1b	nm 62 Type 3a	63 Type 5a
20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40	250 <i>μ</i> Ι	1/200	0.072 0.109 0.279 0.093 0.080 0.251 3 3 3 2.227 0.263 0.071 0.103 0.045 0.045 0.045 0.045 0.045 0.045	0.130 0.293 0.249 0.151 0.266 0.100 1.649 3 3 1.921 0.415 0.172 0.054 0.045 0.045 0.047 0.045 0.047	0.096 0.084 0.172 0.297 0.438 0.457 0.722 2.528 3 2.849 1.424 0.356 0.154 0.096 0.044 0.045 0.045 0.049 0.046 0.047 0.050 0.048	0.051 0.052 0.052 0.054 0.056 0.048 0.066 0.839 2.345 2.580 1.333 0.162 0.064 0.057 0.051 0.046 0.048 0.057 0.048

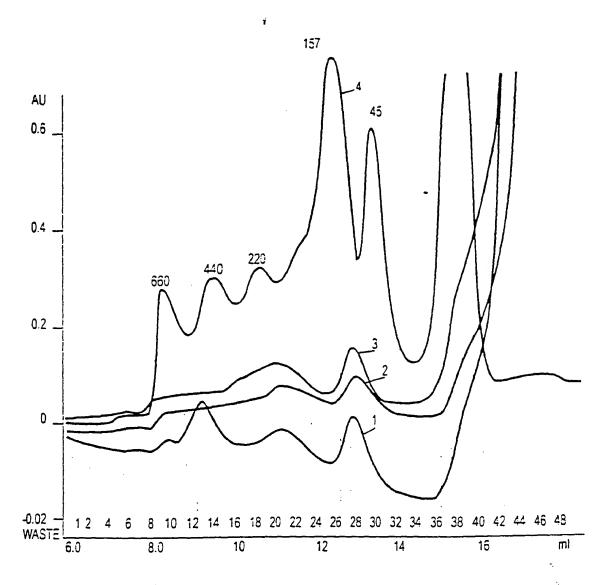


FIGURE 25

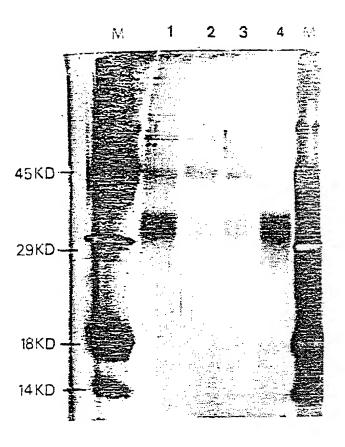


Figure 25

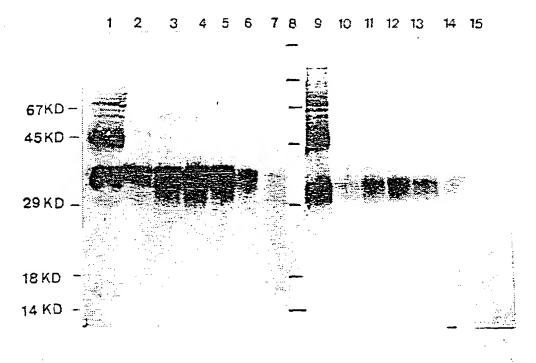


Figure 27

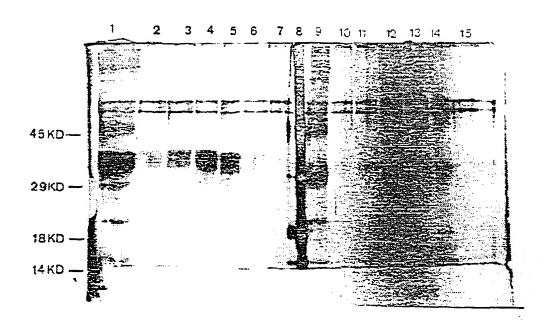
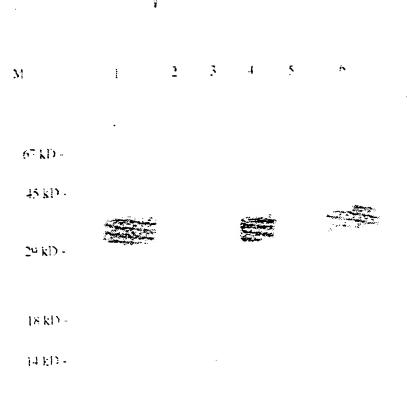


Figure 28



Lane 1: Crude Lysate

Lang 2: Flow through Lentil Chromatography

Lane 3: Wash with EMPIGEN Lentil Chromatography

Lane 4: Eliute Lentil Chromatography

Latte 5; Flow through during concentration lentil cluate

Lanc 6: Pool of Hiafter Size Exclusion Chromatography

Figure 29: Western Blot Analysis with anti-E1 mouse monoclonal 5E1A10

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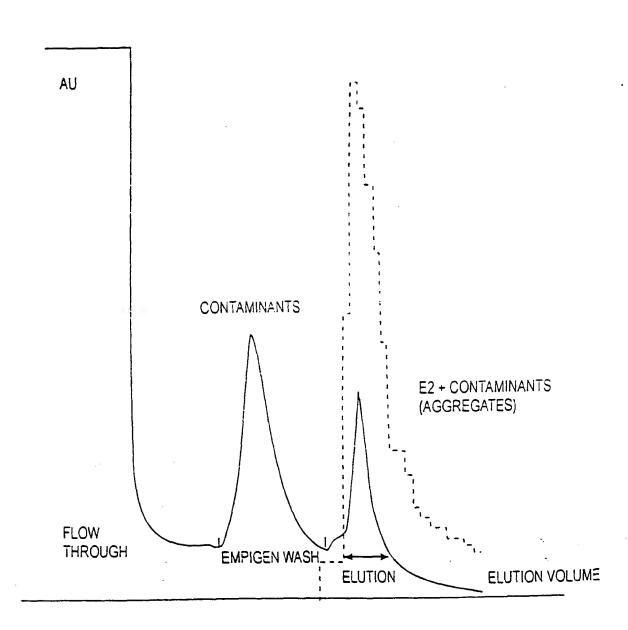
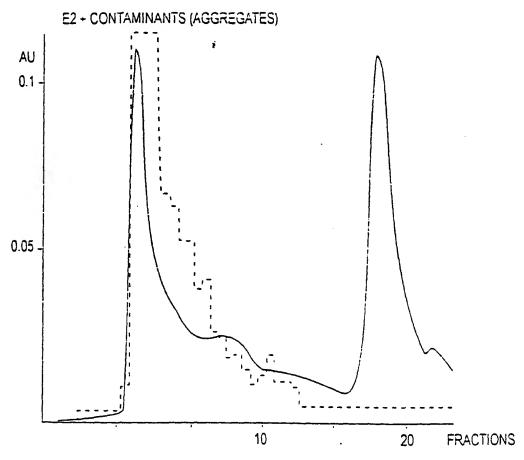


FIGURE 30

A: NON - REDUCED



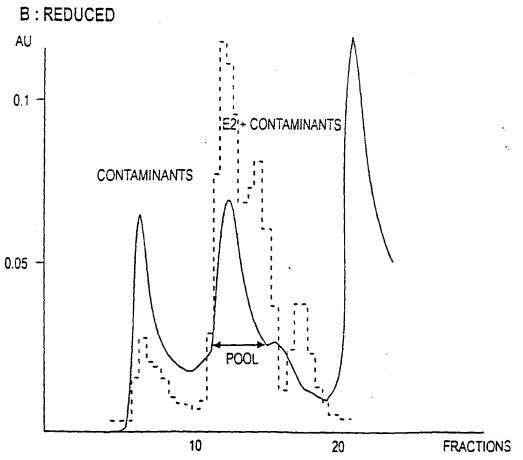


FIGURE 31

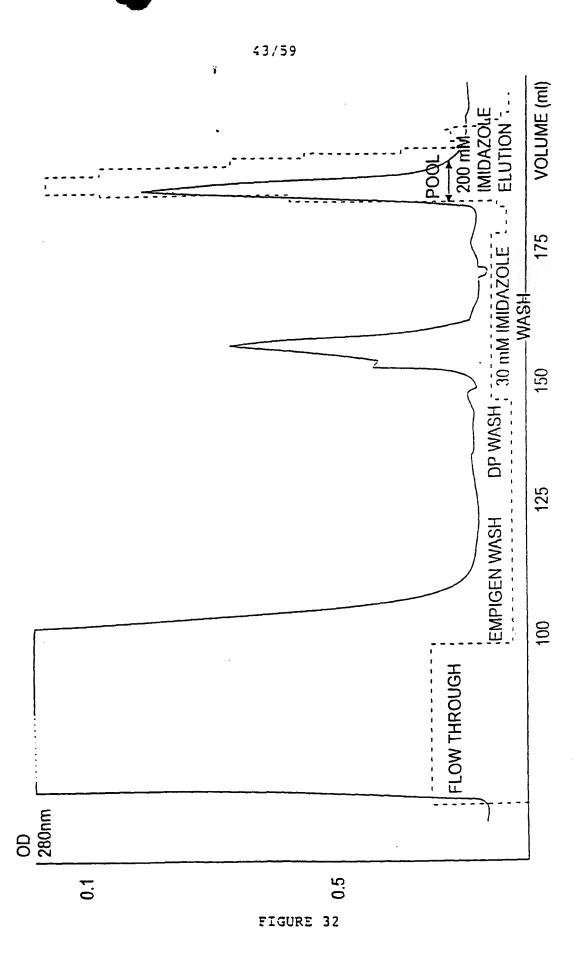
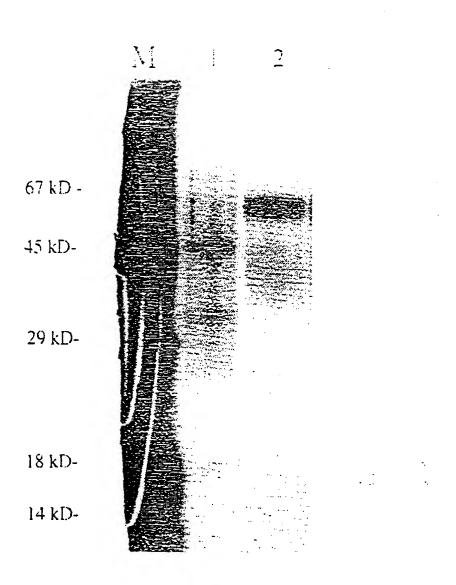
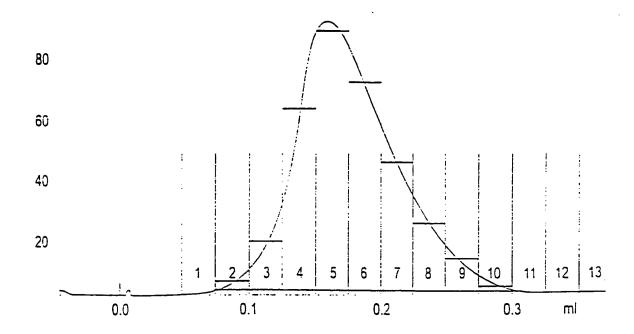


FIGURE 33: SILVER STAIN OF PURIFIED E2



- 1. 30 mM IMIDAZOLE WASH NI-IMAC
- 2. 0.5 ug E2

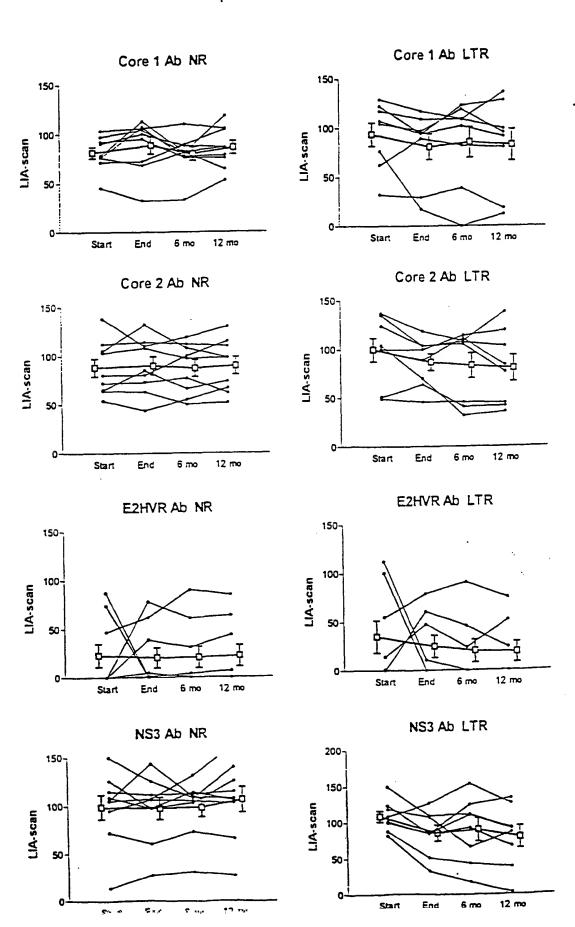
45 59 Figure 34



No.	Ret.	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml≅mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
2	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4
Total Area above baseline = 0.796522 ml*AU
Total area in evaluated peaks = 0.796521 ml*AU
Ratio peak area / total area = 0.999999
Total peak duration = 2.613583 ml







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FIGURE 35B

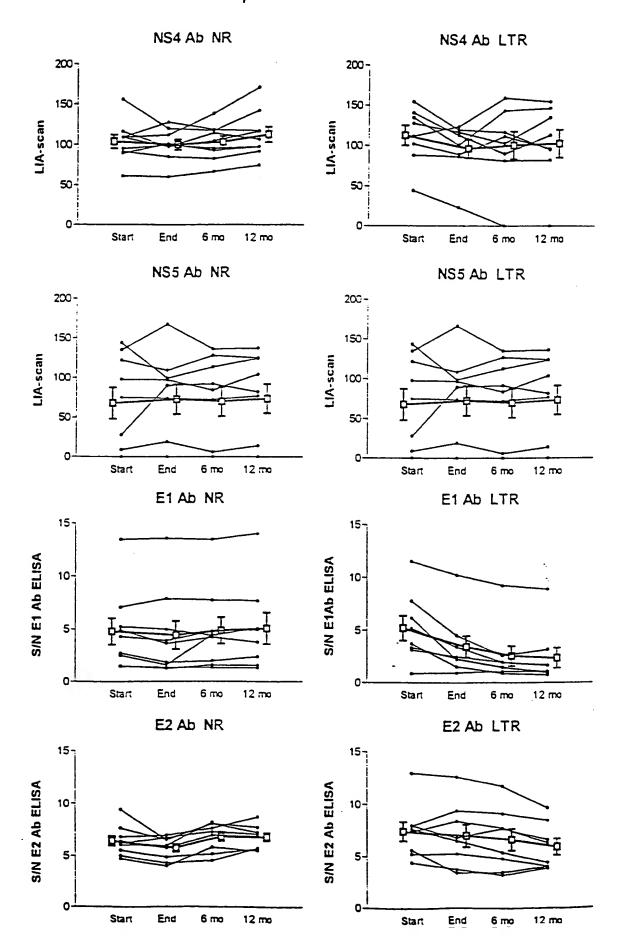
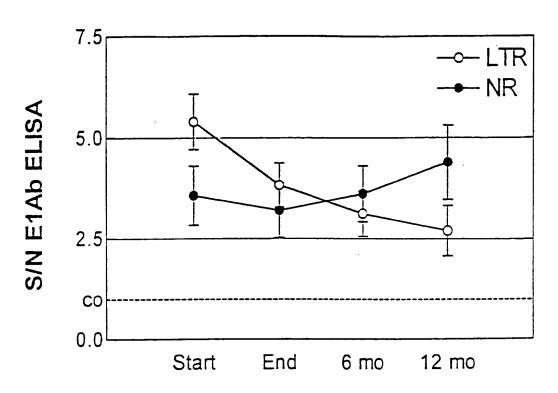


Figure 36

E1 Ab



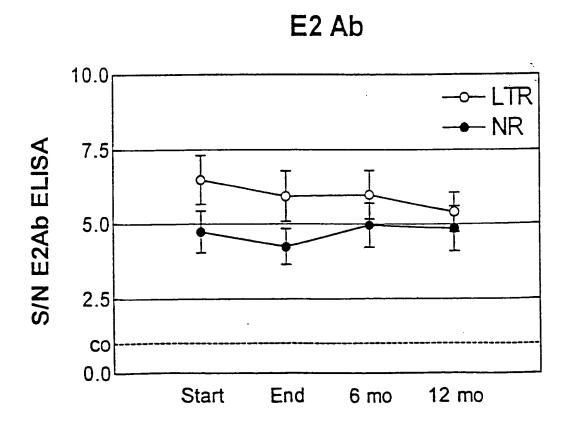


FIGURE 37

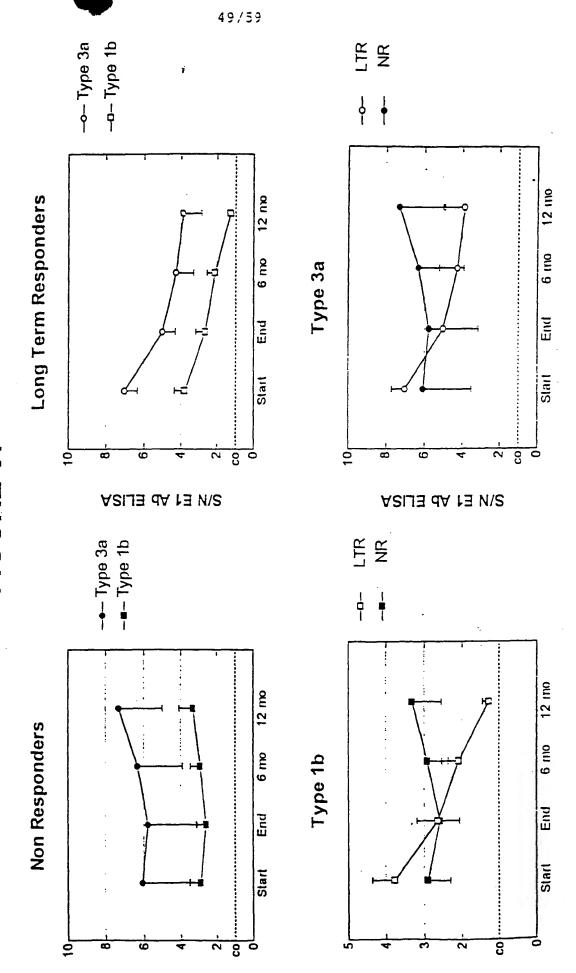
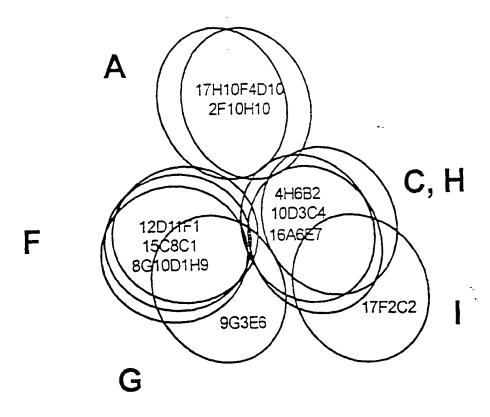


Figure 38

Relative Map Positions of anti-E2 monoclonal antibodies



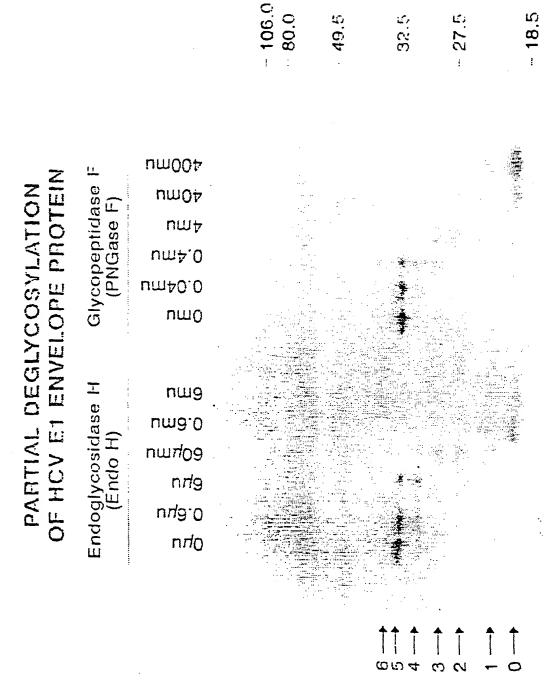


Figure 39

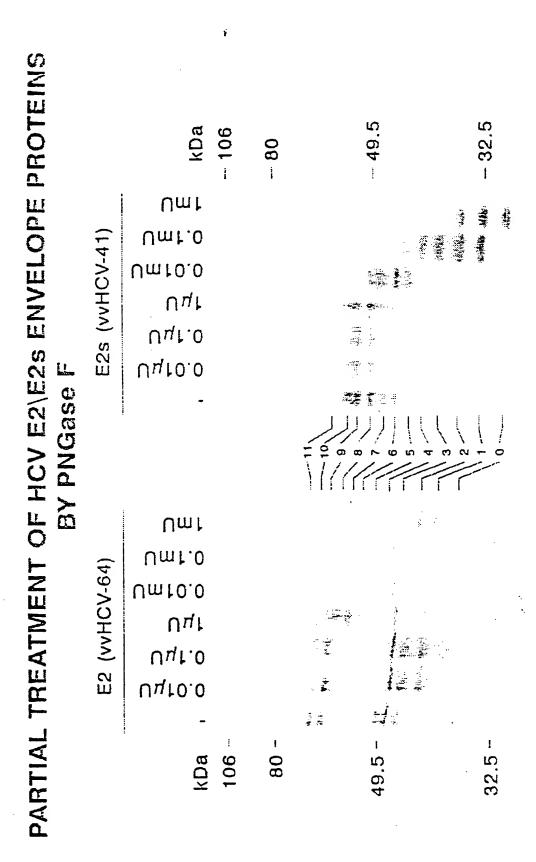


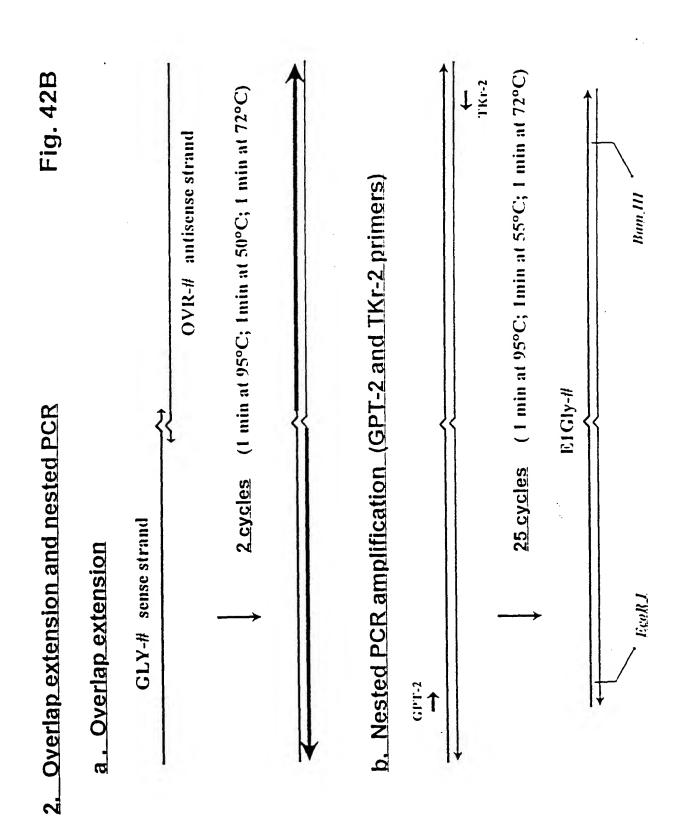
Figure 40

OVR-#

GLY-#

30 cycles (1 min at 95°C; 1 min at 50°C; 1 min at 72°C) In Vitro Mutagenesis of HCV E1 glycoprotein First step of PCR amplification (Gly-# and Ovr-# primers) Bautll \mathbf{E} Uvr-# CIFF CPT Fig. 42A

4



In Vitro Mutagenesis of HCV E1 glycoprotein

Fig. 43

56/59 EIGly-5 EIGly-2 E1Gly-3 E1Gly-1 E1Gly-4 EIGly-6 **E2** Τ₹ 500 m Banell <u>_</u> Bamill 550 nt 6.30 nt <u>-</u> 770 nt **E** OVR-2 GLY-1 Ecok. 1 EcoR. I CORE Ē↑.↓ 10A 82 85 83 84 98 8

	HeLa cells		RK 13 cells		
	2 4 6 1 3 5 7		2 3 4 5 6 2 8 .		
		80,0	•		80.0
_		— 49.5			49.5
	***************************************	32.5	*** ***		32.5
_		— 27.5		_	27.5
		— 18.5			18.5
		1 2 3 5 5 T	1 3 5 7 - 80,0 - 49.5 - 32.5 - 27.5	1 3 5 7 - 80,0 - 49.5 - 32.5 - 27.5	1 2 4 6 7 2 3 5 7 — 80,0 — — — — — — — — — — — — — — — — — —

Figure 44A







Figure 45



Figure 46